Figure 1.

| ri Li | | 1- | 4 | | |
|---|-----|---|-----|----------|--|
| ısage | | | | | |
| a to u | | | | | |
| latio | | | | | |
| in re | | | | | |
| ncies | | | | | |
| freque | | | | | |
| nopo | | 0.37 0.34 0.20 0.04 0.03 | | | |
| wing c | Ser | UCC 0. AGC 0. AGC 0. AGC 0. | 158 | | |
| id sho | | | | | |
| Pro ar | Gln | CAG 0.86 CAA 0.14 | 230 | | |
| -Ser- | | | | | |
| al-Glr | Val | GUU 0.51 GUA 0.26 GUG 0.16 GUC 0.07 | 125 | | |
| -Leu-V | | 9 0 0 8 3 0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | | | |
| e-Lys. | Leu | | 135 | | |
| Ala-Il | | | | | |
| for | Lys | AAA 0.74 AAG 0.26 | 269 | | |
| uences genes | | | | | |
| le seq rial | Ile | AUC 0.83 AUV 0.17 AUA 0.00 | 260 | | |
| leotid bacte | | .35 .26 .10 | | | .17 .15 .08 |
| (a) Nucleotide sequences for Ala-Ile-Lys-Leu-Val-Gln-Ser-Pro and showing codon frequencies in relation to usage in enteric bacterial genes | Ala | GCU 0.35 GCA 0.28 GCG 0.26 GCC 0.10 | 178 | 8 Pro | CCG 0.77 CCA 0.15 CCU 0.08 CCC 0.00 |
| e a | | | | | |

| and showing codon | | | | | | |
|---|-----|--|---------------|--|-----------|--|
| la-Ala-Ser | | | | | | |
| y-Asn-Phe-A | Ser | UCC 0.37 UCU 0.34 AGC 0.20 UCG 0.04 AGU 0.03 UCA 0.02 | Ala | GCM 0.35 GCA 0.28 GCG 0.26 GCC 0.10 50 | | |
| :-Pro-Asn-Gl; snes | Gln | CAG 0.86 CAA 0.14 230 | Ala | GCU 0.35 GCA 0.28 GCG 0.26 GCC 0.10 | | |
| -Val-Gln-Ser oacterial ge | Val | GUU 0.51 GUA 0.26 GUG 0.16 GUC 0.07 | Phe | UUC 0.76 UUU 0.24 | | |
| [le-Lys-Leu· in enteric } | ren | CUG 0.83 CUC 0.07 CUU 0.04 UUG 0.03 UUA 0.02 CUA 0.00 | Asn | AAC 0.94 AAU 0.06 88 | | |
| is for Ala-1 i to usage | Lys | AAA 0.74 AAG 0.26 269 | Gly | GGU 0.59 GGC 0.38 GGG 0.02 GGA 0.00 | | |
| le sequence in relation | Ile | AUC 0.83 AUU 0.17 AUA 0.00 | Asn | AAC 0.94 AAU 0.06 396 | | |
| (b) Nucleotide sequences for Ala-Ile-Lys-Leu-Val-Gln-Ser-Pro-Asn-Gly-Asn-Phe-Ala-Ala-Ser frequencies in relation to usage in enteric bacterial genes | Ala | GCU 0.35 GCA 0.28 GCG 0.26 GCC 0.10 | 8 - 14 Pro | CCG 0.77 CCA 0.15 CCU 0.08 CCC 0.00 | 15 Ser | UCC 0.37 UCU 0.34 AGC 0.20 UCG 0.04 AGU 0.03 UCA 0.02 |

| • | 3/4 | | | | | | | |
|---|--|------------|---------------|----------------------------------|-----------------|----------------|--|----------|
| -Asp-Gly-Thr- acterial genes. | | | | · | | | | |
| r-Phe-Val-Leu : in enteric b | | | | | | | | |
| (c)Nucleotide sequences for Ala-Ile-Lys-Leu-Val-Gln-Ser-Pro-Asn-Gly-Asn-Phe-Ala-Ala-Ser-Phe-Val-Leu-Asp-Gly-Thr- Lys-Trp-Ile-Phe-Lys-Ser-Lys-Tyr and showing codon frequencies in relation to usage in enteric bacterial gene Ala Ile Lys Leu Val Gln | 0.34 0.02 0.04 0.03 | · · · | ιζ | | 0.10 | <u>н</u> | 0.55 0.35 0.07 0.04 | |
| -Asn-Pl n relat ser | HCC HCC HCC HCC HCC | | Ala | 900 900 900 900 900 | 900 50 | Thr | ACC ACC ACC | 338 |
| .Pro-Asn-Gly cequencies i Gln | CAG 0.86 CAA 0.14 | 230 | Ala | GCU 0.35 GCA 0.28 GCG 0.26 | | Gly | GGU 0.59 GGC 0.38 GGG 0.02 GGA 0.00 | 240 |
| al-Gln-Ser. ng codon fi Val | GUU 0.51 GUA 0.26 GUG 0.16 GUC 0.07 | 125 | Phe | UUC 0.76 | 34 | Asp | GAC 0.67 GAU 0.33 | 161 |
| e-Lys-Leu-V r and showi Leu | CUG 0.83 CUC 0.07 CUU 0.04 UUG 0.03 | 135 135 | Asn | AAC 0.94 AAU 0.06 | 88 | ren | CUG 0.83 CUC 0.07 CUU 0.04 UUG 0.03 | CUA 0.00 |
| for Ala-Il -Lys-Tyr-Ty Lys | AAA 0.74 AAG 0.26 | 269 | Gly | GGU 0.59 GGC 0.38 GGG 0.02 | GGA 0.00 148 | Val | GUU 0.51 GUA 0.26 GUG 0.16 GUC 0.07 | 167 |
| e sequences Phe-Lys-Ser Ile | AUC 0.83 AUU 0.17 AUA 0.00 | 260 | Asn | AAC 0.94 AAU 0.06 | 396 | - Bhe | UUC 0.76 UUU 0.24 | 216 |
| (c)Nucleotide sequences for Ala-Ile Lys-Trp-Ile-Phe-Lys-Ser-Lys-Tyr-Tyr Ala Ile Lys | GCU 0.35 GCA 0.28 GCG 0.26 | 178 | 8 - 14 Pro | CCG 0.77 CCA 0.15 | | 15 - 21 Ser | UCC 0.37 UCU 0.34 AGC 0.20 UCG 0.04 | |

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| Lys | AAA 0.74 AAG 0.26 | o | | | |
|---------|--|-----------------------------|----------------|----------|---|
| Ser | UCC 0.37 UCU 0.34 AGC 0.20 UCG 0.04 | AGU 0.02 UCA 0.02 154 | | | |
| Lys | AAA 0.74 AAG 0.26 | 152 | | | |
| Phe | UUC 0.76 UUU 0.24 | 154 | | | |
| Ile | AUC 0.83 AUU 0.17 AUA 0.00 | 173 | | | |
| £ | UGG 1.00 | 467 | Tyr | UAC 0.75 | 0 |
| 22 - 28 | AAA 0.74 AAG 0.26 | 467 | 29 - 30 Tyr | UAC 0.75 | 0 |